AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A method ~~Method~~ for assessing *in vitro* the predisposition of a subject to develop cardiovascular pathologies, ~~characterized in that the identity of~~ comprising identifying the nucleotide corresponding to position 436 of seq IDN1 (COX-2 gene PROMOTER) ~~is established~~ on a sample of genomic DNA of said subject[[)]].

2. **(Currently amended)** The method ~~Method~~ according to claim 1, where the genomic DNA is extracted from cells of such subject, derived from blood samples, saliva, biopsies, urine, human tissue.

3. **(Currently amended)** The method ~~Method~~ according to claim 2, where said cardiovascular pathologies are caused by or associated with rupture of an atherosclerotic plaque.

4. **(Currently amended)** The method ~~Method~~ according to Claim 1 ~~claims 1-3~~, ~~where such~~ wherein said cardiovascular pathologies are coronaropathies, pathologies of carotid arteries, myocardial infarction, angina pectoris, acute coronary syndromes, myocardial revascularization by means of coronary by-pass or angioplasty, stroke, transient ischemic attack (TIA), peripheral arteriopathy, trombophylic syndromes.

5. **(Currently amended)** The method ~~Method~~ according to claim 4, ~~where such~~ wherein said identification ~~assessment~~ is ~~made~~ carried out by one of the following techniques: sequencing, endonuclease digestion with restriction enzymes, selective hybridization with oligonucleotides specific for polymorphism at position -765 of the human COX-2 gene promoter, ~~methodology of~~ single strand conformational polymorphism (SSCP), DGGE, Fluorescence assisted mismatch analysis (FAMA), heteroduplex analysis, Real Time PCR.

6. **(Currently amended)** The method ~~Method~~ according to claim 5, wherein said ~~assessment is made~~ identification is carried out by endonuclease digestion with restriction enzymes.

7. **(Currently amended)** The method ~~Method~~ according to claim 6, comprising the following steps:

- ~~extraction of~~ extracting genomic DNA from a biological sample of the subject,
- ~~amplification~~ amplifying by means of Polymerase Chain Reaction with oligonucleotides or primers suitable for ~~amplication~~ amplification of a DNA fragment comprising position -765,

- ~~enzymatic digestion of~~ enzymatically digesting such amplified fragment with a restriction enzyme selected from: Fau I and Aci I

- ~~electrophoretic separation of~~ electrophoretically separating the restriction mixture comprising the restriction fragments or of the undigested amplified fragment, or of both,

- ~~analysis of~~ analyzing the restriction profile generated after visualization of DNA.

8. **(Currently amended)** The method ~~Method~~ according to claim 7, ~~characterized in that the~~ wherein said amplifying ~~amplification~~ is carried out with ~~oligonucleotidies~~ oligonucleotides having sequences at least partially identical to sequences ID NO 3 and ID NO 4 and the amplified fragment is digested with the restriction enzyme Fau I.

9. **(Currently amended)** The method ~~Method~~ according to claim 8, ~~characterized in that the~~ wherein said amplifying ~~amplification~~ is carried out with oligonucleotides having sequence SEQ. ID NO 3 and 4.

10. **(Currently amended)** The method ~~Method~~ according to claim 1 ~~claims 1-9~~, ~~characterized in that~~ wherein the presence of a cytosine (C) at position 436 of SEQ ID NO: 1 ~~IDN1~~, in at least one DNA allele of such subject, indicates a lower risk to predisposition to cardiovascular diseases than the risk associated to the presence of a guanosine (G) in position 436 on both alleles.

11. **(Currently amended)** A kit ~~Kit in order to carry~~ for carrying out the method according to claim 1 ~~claims 1-10~~.

12. **(Currently amended)** The kit ~~Kit~~ according to claim 11, ~~characterized for~~ comprising at least one of the following oligonucleotides: an oligonucleotide comprising at least 10 consecutive nucleotides of seq ID NO 3, an oligonucleotide comprising at least consecutive nucleotides of seq ID NO 4 and optionally one restriction enzyme selected from: Fau I and Aci I.

13. **(Currently amended)** The kit ~~Kit~~ according to claim 12, comprising the oligonucleotide with sequence ID NO 3 and the oligonucleotide with sequence ID NO 4, the Fau I restriction enzyme and optionally one molecular weight DNA standard.

14. **(Currently amended)** A prognostic method ~~Use of the genotyping of nucleotide at position 436 of seq IDN1 (COX-2 gene promoter) for the preparation of a prognostic tests~~ for a cardiovascular pathology selected from the group consisting of: coronaropathies, pathologies of

carotid arteries, myocardial infarction, angina pectoris, acute coronary syndromes, myocardial revascularization by means of coronary by-pass or angioplasty, stroke, transient ischemic attack (TIA), peripheral arteriopathy, and trombophilic syndromes, comprising genotyping of nucleotide at position 436 of SEQ ID NO: 1 (COX-2 gene promotor).

15. **(Currently amended)** A method of assessing the sensitivity to therapy with non steroidal anti-inflammatory drugs (NSAIDs) comprising genotyping ~~Use of the genotypzation~~ of nucleotide at position 436 of SEQ ID NO: 1 ~~seq IDN1~~ (COX-2 gene promotor) ~~to prepare diagnostic tests for the sensitivity to therapy with non steroidal anti-inflammatory drugs (FANS)~~.

16. **(New)** The kit for carrying out the method according to claim 10.

17. **(New)** The method according to claim 16 wherein the presence of a cytosine (C) at position 436 of SEQ ID NO: 1, in at least one DNA allele of such subject, indicates a lower sensitivity to therapy with non steroidal anti-inflammatory drugs (NSAIDs) than the presence of a guanosine (G) in position 436 on both alleles.

18. **(New)** A kit for assessing the sensitivity to therapy with non steroidal anti-inflammatory drugs (NSAIDs) comprising genotyping a nucleotide at position 436 of SEQ ID NO: 1 (COX-2 gene promotor) with suitable oligonucleotides.

19. **(New)** A kit according to claim 18 comprising the oligonucleotides having SEQ ID NO: 3 and SEQ ID NO: 4.